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JUN 21 2001

TECH CENTER 1600/2900

1614

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/754,167

DATE: 05/16/2001

TIME: 09:43:15

ENTERED

Input Set : A:\RTS-0140_Seq_ASCII.txt

Output Set: N:\CRF3\05162001\I754167.raw

```

6 <110> APPLICANT: Brett P. Monia
7   Jacqueline Wyatt
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 1 EXPRESSION
11 <130> FILE REFERENCE: RTS-0140
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/754,167
14 <141> CURRENT FILING DATE: 2000-12-19
16 <160> NUMBER OF SEQ ID NOS: 87
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 20
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Antisense Oligonucleotide
27 <400> SEQUENCE: 1
28 tccgtcatcg ctccctcaggg
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 20
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Antisense Oligonucleotide
39 <400> SEQUENCE: 2
40 atgcattctg cccccaagga
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 2091
45 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (64)...(1512)
52 <400> SEQUENCE: 3
53 gagcggagcc gcgggcgagg gggcggaagg accgactgac ggtagggacg ggagggcgagc 60
55 aag atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac 108
56 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr
57 1 5 10 15
59 gac ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag 156
60 Asp Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys
61 20 25 30
63 cct cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc 204
64 Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu
65 35 40 45
67 tac cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag 252
68 Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu
69 50 55 60
71 atg acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc 300
72 Met Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile
73 65 70 75

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RECEIVED
JUN 22 2001
Technology Center 2100

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75 cgt cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac      348
76 Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn
77 80      85      90      95
79 gtt ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag      396
80 Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln
81      100      105      110
83 ttg tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag      444
84 Leu Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln
85      115      120      125
87 cag acg gac atc gct gtg aat tgg gct ggc ggc ctg cac cat gca aag      492
88 Gln Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys
89      130      135      140
91 aag tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc      540
92 Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala
93      145      150      155
95 atc ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att      588
96 Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile
97 160      165      170      175
99 gat att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac      636
100 Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp
101      180      185      190
103 cgg gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga      684
104 Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly
105      195      200      205
107 act ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct      732
108 Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala
109      210      215      220
111 gtt aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc      780
112 Val Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala
113      225      230      235
115 att ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt      828
116 Ile Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser
117 240      245      250      255
119 gcg gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta      876
120 Ala Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu
121      260      265      270
123 ggt tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt      924
124 Gly Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe
125      275      280      285
127 gtc aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac      972
128 Val Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr
129      290      295      300
131 acc att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc      1020
132 Thr Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala
133      305      310      315
135 ctg gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa      1068
136 Leu Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu
137 320      325      330      335
139 tac ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act      1116

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140 Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr
141          340          345          350
143 aac cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt 1164
144 Asn Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe
145          355          360          365
147 gag aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg 1212
148 Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala
149          370          375          380
151 att cct gag gag gcc atc cct gag gag agt ggc gat gag gac gaa gac 1260
152 Ile Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp
153          385          390          395
155 gac cct gac aag cgc atc tcg atc tgc tcc tct gac aaa cga att gcc 1308
156 Asp Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala
157 400          405          410          415
159 tgt gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc 1356
160 Cys Glu Glu Glu Phe Ser Asp Ser Glu Glu Gly Glu Gly Gly Arg
161          420          425          430
163 aag aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat 1404
164 Lys Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp
165          435          440          445
167 gaa aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag 1452
168 Glu Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu
169          450          455          460
171 aaa acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc 1500
172 Lys Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val
173          465          470          475
175 aag ttg gcc tga atggacctct ccagctctgg ctctctgctg agtccctcac 1552
176 Lys Leu Ala
177 480
179 gtttcttccc caaccctca gattttatat tttctatttc tctgtgtatt tatataaaaa 1612
181 tttattaaat ataaatatcc ccagggacag aaaccaaggc cccgagctca gggcagctgt 1672
183 gctgggtgag ctcttccagg agccaccttg ccacccattc ttcccgttct taactttgaa 1732
185 ccataaaggg tgccaggctct gggtgaaagg gatactttta tgcaaccata agacaaactc 1792
187 ctgaaatgcc aagtgcctgc ttagtagctt tggaaagggtg cccttattga acattctaga 1852
189 aggggtggct gggctctcaa ggatctcctg tttttttcag gtcctaaag taacatcagc 1912
191 cttttttaga ttggttctgt tttcgtacct tccactggc ctcaagtga ccaagaaaca 1972
193 ctgcctgccc tctgtctgtc ttctcctaatt tctgcagggtg gaggttgcta gtctagtttc 2032
195 ctttttgaga tactattttc atttttgtga gcctotttgt aataaaatgg tacatttct 2091
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199 <211> LENGTH: 19
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: PCR Primer
206 <400> SEQUENCE: 4
207 accttccac tggcctcaa 19
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 24
212 <212> TYPE: DNA

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213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: PCR Primer
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219 cacctgcaga attaggagaa gaca 24
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223 <211> LENGTH: 26
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR Probe
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231 agccaagaaa cactgcctgc cctctg 26
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 21
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Primer
242 <400> SEQUENCE: 7
243 caacggattt ggtcgtattg g. 21
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247 <211> LENGTH: 26
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: PCR Primer
254 <400> SEQUENCE: 8
255 ggcaacaata tccactttac cagagt 26
258 <210> SEQ ID NO: 9
259 <211> LENGTH: 21
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: PCR Probe
266 <400> SEQUENCE: 9
267 cgcctggtca ccagggtgc t 21
270 <210> SEQ ID NO: 10
271 <211> LENGTH: 20
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
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278 <400> SEQUENCE: 10
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283 <211> LENGTH: 20
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence

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288 <223> OTHER INFORMATION: Antisense Oligonucleotide
290 <400> SEQUENCE: 11
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295 <211> LENGTH: 20
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Antisense Oligonucleotide
302 <400> SEQUENCE: 12
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307 <211> LENGTH: 20
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Antisense Oligonucleotide
314 <400> SEQUENCE: 13
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319 <211> LENGTH: 20
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Antisense Oligonucleotide
326 <400> SEQUENCE: 14
327 ccatagttga gcagcaaatt                                20
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331 <211> LENGTH: 20
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Antisense Oligonucleotide
338 <400> SEQUENCE: 15
339 agagaccata gttgagcagc                                20
342 <210> SEQ ID NO: 16
343 <211> LENGTH: 20
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
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350 <400> SEQUENCE: 16
351 tcggtagaga ccatagttga                                20
354 <210> SEQ ID NO: 17
355 <211> LENGTH: 20
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number